SEQUENCE LISTING

<110> Fuso Pharmaceutical Industries Ltd.

<120> Novel serine protease BSSP5

<130> 661640

<150> JP 10-347806

<151> 1998-11-20

<160> 32

<210> 1

<211> 1149

<212> DNA

<213> human

<400> 1

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                -30                 -25                 -20

tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc ttc agc cag agg  109
Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln Arg
        -15                 -10                 -5                  -1

att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg ccc tgg cag gtg tcc  160
Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln Val Ser
  1                 5                  10                  15
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ctg cag gac agc agc ggc ttc cac ttc tgc ggt ggt tct ctc atc agc cag 211
Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Gln
20 25 30

tcc tgg gtg gtc act gct gcc cac tgc aat gtc agc cct ggc cgc cat ttt 262
Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro Gly Arg His Phe
35 40 45 50

gtt gtc ctg ggc gag tat gac cga tca tca aac gca gag ccc ttg cag gtt 313
Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Leu Gln Val
55 60 65

ctg tcc gtc tct cgg gcc att aca cac cct agc tgg aac tct acc acc atg 364
Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser Trp Asn Ser Thr Thr Met
70 75 80 85

aac aat gac gtg acg ctg ctg aag ctc gcc tcg cca gcc cag tac aca aca 415
Asn Asn Asp Val Thr Leu Leu Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr
90 95 100

cgc atc tcg cca gtt tgc ctg gca tcc tca aac gag gct ctg act gaa ggc 466
Arg Ile Ser Pro Val Cys Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly
105 110 115

ctc acg tgt gtc acc acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg 517
Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val
120 125 130 135

aca cca gca cat ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag 568
Thr Pro Ala His Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln
140 145 150

tgc cgg cag tac tgg gac tca agt atc act gac tcc atg atc tgt gca ggt 619

Cys Arg Gln Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly

155 160 165 170

ggc gca ggt gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc 670

Gly Ala Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys

175 180 185

cag aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa 721

Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys

190 195 200

aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc agc 772

Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser

205 210 215 220

acc tgg atc aac cag gtc ata gcc tac aac tga gctcaccaca ggccctcccc 825

Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn

225 230

agctcaaccc atttaaagga cccaggccct gtcccatcat gcattcatgt ctgtcttcct 885

ggctcaggag aaagaagagg ctgttgaggg tccgactccc tacttggact tctggcacag 945

aaggggctga gtgactcctt gagtagcagt ggctcttcct agagtagcca tgccgtggcc 1005

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<210> 2

<211> 264

<212> PRT

<213> human

<400> 2

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        -15                 -10                 -5              -1
Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln Val Ser
  1               5                  10                  15
Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Gln
          20                  25                  30
Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro Gly Arg His Phe
 35                  40                  45                  50
Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Leu Gln Val
              55                  60                  65
Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser Trp Asn Ser Thr Thr Met
     70                  75                  80                  85
Asn Asn Asp Val Thr Leu Leu Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr
                 90                  95                 100
Arg Ile Ser Pro Val Cys Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly
         105                 110                 115
Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val
120                 125                 130                 135
Thr Pro Ala His Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln
             140                 145                 150
Cys Arg Gln Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly
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155 160 165 170

Gly Ala Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys

175 180 185

Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys

190 195 200

Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser

205 210 215 220

Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn

225 230

<210> 3

<211> 834

<212> DNA

<213> mouse

<400> 3

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-30

agc ctg gtc ctc ctt ggc tcc tcc tgg ggc tgt ggt gtt cct gcc atc acg 107

Ser Leu Val Leu Leu Gly Ser Ser Trp Gly Cys Gly Val Pro Ala Ile Thr

-25 -20 -15 -10

cct gca ctg agc tac aat cag aga att gtc aac ggg gag aat gca gtg cca 158

Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn Ala Val Pro

-5 -1 1 5

ggc tcc tgg ccc tgg cag gtg tct ctc cag gat aac acc ggc ttc cac ttc 209
Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe
10 15 20 25

tgc ggt ggt tct ctc atc agt ccg aac tgg gtg gtc acg gct gcc cac tgc 260
Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys
30 35 40

caa gtc acg cct gga cgc cac ttt gtc gtt ttg gga gaa tat gac cga tct 311
Gln Val Thr Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
45 50 55 60

tcc aat gct gaa cct gtg cag gtc ctc tcg atc gca agg gcc atc aca cac 362
Ser Asn Ala Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His
65 70 75

cct aac tgg aac gcc aac acc atg aac aat gac ctg act ctc ctg aag ctt 413
Pro Asn Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu
80 85 90

gcc tcg cca gcc cgg tac aca gca caa gtc tca cca gtc tgc ctg gct tcc 464
Ala Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser
95 100 105 110

aca aac gag gca ctg cct tcg ggg ctc acc tgt gtc acc act ggc tgg ggc 515
Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp Gly
115 120 125

cga atc agt ggt gtg ggc aat gtg aca cca gct cgc ctg cag caa gtt gtt 566
Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val
130 135 140 145

cta ccc ctg gtc act gtg aat cag tgt cgg cag tac tgg ggt gca cgc att 617

Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile
150 155 160

acc gat gcc atg ata tgt gca ggt ggc tca ggc gcc tcc tca tgt cag ggt 668
Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly
165 170 175

gac tca gga ggc cct ctt gtc tgc cag aag gga aac acc tgg gtg ctt att 719
Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile
180 185 190 195

ggg att gtc tcc tgg ggc act aag aac tgc aac ata caa gca ccg gcc atg 770
Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met
200 205 210

tac act cgg gtc agc aag ttc agt acc tgg atc aac caa gtc atg gcc tac 821
Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp Ile Asn Gln Val Met Ala Tyr
215 220 225 230

aac taaactgtcc 834
Asn

<210> 4

<211> 264

<212> PRT

<213> mouse

<400> 4

Met Leu Leu Leu Ser Leu Thr Leu
-30

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-25                 -20                 -15                 -10
Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn Ala Val Pro
            -5              -1  1               5
Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe
 10                  15                  20                  25
Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys
            30                  35                  40
Gln Val Thr Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
     45                  50                  55                  60
Ser Asn Ala Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His
                65                  70                  75
Pro Asn Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu
         80                  85                  90
Ala Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser
 95                  100                 105                 110
Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp Gly
            115                 120                 125
Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val
     130                 135                 140                 145
Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile
                150                 155                 160
Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly
         165                 170                 175
Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile
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180 185 190 195

Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met

200 205 210

Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp Ile Asn Gln Val Met Ala Tyr

215 220 225 230

Asn

<210> 5

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 5

aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60 tgctgccccc

tttgacgacg atgacaagga tccgaattc 99

<210> 6

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

<400> 6

gaattcggat ccttgtcatc gtcgtcaaag ggggcagcaa cagcagcagc aacaaaggta 60 aggatcagga

gtagattcat ggtgttgcta gccaagctt 99

<210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 7

ttggtgcatg gcgga 15

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 8

tcctcgagac ttggcctgaa tggtttt 27

<210> 9

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin

<400> 9

gcgctagcag atctccatga atctactcct gatcc 35

<210> 10

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pSecTrypHis/Neurosin

<400> 10

tgaagcttgc catggaccaa cttgtcatc 29

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypHis

<400> 11

ccaagcttca ccatcaccat caccat 26

<210> 12

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypSigTag

<400> 12

gcacagtcga ggctgat 17

<210> 13

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid pFBTrypSigTag

<400> 13

caaatgtggt atggctg 17

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify conserved region of serin proteases-encoding sequence

<220>

<221> UNSURE

<220> 9, 12

<223> n is a, c, g or t.

<400> 14

gtgctcacng cngcbcaytg 20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify conserved region of serin proteases-encoding sequence

<220>

<221> UNSURE

<220> 12, 15

<223> n is a, c, g or t.

<400> 15

ccvctrwsdc cnccnggcga 20

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (forward)

<400> 16

tgtcagccct ggccgccatt 20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (forward)

<400> 17

gcgagtatga ccgatcatca 20

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse)

<400> 18

cgccacctgc acagatcatg 20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse)

<400> 19

gaatcagtgc cggcagtact 20

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP5F1 to amplify full length hBSSP5 (forward)

<400> 20

tgccacgatg ttgctgctca 20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP5F2 to amplify mature hBSSP5-encoding region (forward)

<400> 21

attgtcaacg gggagaatgc 20

<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP5R1/E to amplify full length hBSSP5 (reverse)

<400> 22

ggaattcggg tctttaatgg gttgagc 27

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as hBSSP5R4 for RT-PCR (reverse)

<400> 23

cctggcacga ggaggcac 18

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5F1 for RACE for mBSSP5 (forward)

<400> 24

accatgaaca atgacctgac 20

<210> 25

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5F2 for RACE for mBSSP5 (forward)

<400> 25

gaatcagtgt cggcagt 17

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5F3 to amplify full length mBSSP5 (forward)

<400> 26

gaccatctca acaccattcc 20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5Fmature to amplify mature mBSSP5-encoding region (forward)

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<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5.1 for RACE for mBSSP5 (reverse)

<400> 28

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<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5R2 for RACE for mBSSP5 (reverse)

<400> 29

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<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer designated as mBSSP5R3/E to amplify full length mBSSP5 (reverse)

<400> 30

ggaattcgga cagtttagtt gtaggcc 27

<210> 31

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 31

aagcttggct agcaacacca tgaatctact cctgatcctt acctttgttg ctgctgctgt 60

tgctgccccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

<210> 32

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

<400> 32

gaattcggat ccttgtcatc gtcgtcatgg tgatggtgat ggtgaaaggg ggcagcaaca 60

gcagcagcaa caaaggtaag gatcaggagt agattcatgg tgttgctagc caagctt 117